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Conformational polymorphism of D-sorbitol (D-glucitol): the crystal and molecular structures of D-glucitol 2/3-hydrate and *epsilon* D-glucitol

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Abstract

The crystal structures of D-glucitol 2/3-hydrate (**1**) and *epsilon* D-glucitol (**2**) were determined by X-ray crystallography and refined to final conventional parameters of $R = 0.034$ and 0.050, respectively. The conformations of the three independent molecules of **1** and one of the two independent molecules of **2** are similar and exhibit, bent-chain, sickle conformations of the carbon chain, thus avoiding the unfavourable 1,3-parallel O//O interactions. However, the orientation of a terminal hydroxyl group differs from the one observed in the bent-chain conformation of the known *A* form. An even more striking observation is the unexpected, extended, zigzag conformation of the second independent molecule of **2**, which results in a 1,3-parallel interaction between O-2 and O-4. Thus in the class of alditols, the crystals of the *epsilon* and *A* forms of D-glucitol constitute the rarely occurring type of *conformational* polymorphism. © 1998 Elsevier Science Ltd. All rights reserved

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1. Introduction

From powder diffraction data [1,2], it is known that several polymorphs of D-sorbitol (the hexitol D-glucitol, or L-gulitol), one of the most widely used ingredients in both pharmaceutical and food preparations, do exist. In literature such data have been reported for the *beta*, *gamma*, *delta* and *epsilon* forms, but no information on single crystal analyses of these forms is available. The crystal structures of the *A* form [2] and the glucitol–pyridine complex [3] have been reported in 1971. The Cambridge Structural Database [4] contains the crystal structures of all possible diastereoisomers of the alditols up to and including the heptitols: the

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two tetritols, the three pentitols, the six hexitols and the ten heptitols. The rotational flexibility about the C–C bonds in the polyhydroxyalkyl chain of alditols (sugar alcohols) gives rise to a mixture of many rotamers in solution. This mixture is presumed to consist mainly of those molecules in which the vicinal interactions are staggered with an energy barrier, for passing through the eclipsed conformation, that is low enough to permit interconversion in solution at room temperature. A major contribution to the variety of possible rotamers is provided by the staggered orientations of the terminal hydroxyl groups which are susceptible to environmental effects. One may safely assume that conformational heterogeneity in solution tends to inhibit crystallization. However, in polar solvents, additional solvation effects like hydrogen bonding to a functional group of the solvent could significantly influence the rotamer distribution.

Jeffrey [5] has pointed out that alditols provide a clear example of a single conformation in the crystal going to multiple conformations in solution. This phenomenon results in very low molecular optical rotations [5,6]. Though the rotamer distribution might be expected to yield crystals exhibiting *conformational polymorphism* [7], this has so far not been observed in unsubstituted alditols. Polymorphism of a more common type has been reported for D-mannitol [8,9], which displays similar conformations in three different crystal structures.

On stereochemical basis, it has been pointed out [5,7] that the solid-state conformation of the pentitols and at least up to the hexitols can be predicted from the configuration at each chiral carbon atom along the chain. The carbon chain adopts the extended, planar zigzag conformation when the configurations at alternate carbon centers are different (DL-arabinitol, D-mannitol and galactitol), and is bent and non-planar when they are the same. It was for a long time the almost generally accepted opinion that the carbon chain in unsubstituted alditols in crystals had to bend to a sickle in those cases where a planar carbon chain would give rise to parallel 1,3-*peri* C(n)–O//C(n + 2)–O interactions. Moreover, bent-chain, so-called sickle conformations can also give rise to parallel 1,3-peri arrangements of C(n)–C and C(n + 2)–O bonds. Angyal et al. [10] reported that conformations containing parallel C//O interactions are frequently more stable than those with parallel O//O interactions. Given ideal distances and angles, the separation of alternate oxygen atoms is 2.50 Å and this 1,3-interaction has an estimated instability factor of about 8 kJ/mole [7,10]. Due to steric and electrostatic repulsion, rotamers having these *peri* interactions should therefore be energetically less favourable, resulting in a small population of these conformers in solution. This might be of importance in the process of crystallization. Nevertheless, these relatively unfavourable conformations do occasionally occur in the solid state and surprisingly are not always avoided by simple 120° rotations about C–C bonds. Recently, it was reported that 1,3-parallel C//O arrangements in sickle conformations as well as 1,3-parallel O//O orientations in extended chains are tolerated none the less [11–13]. In the reported alditol crystal structures, no parallel O//O or C//O contacts occur in tetritols and pentitols. In hexitols, only D-altritol has a C//O contact. In the class of heptitols, C//O contacts are present in *meso-glycero-allo*-heptitol, D-*glycero*-L-*allo*-heptitol and D-*glycero*-D-*manno*-heptitol and only one heptitol (*meso*-D-*glycero*-L-*altro*-heptitol) shows an O//O contact.

In an attempt to predict crystal structures of simple carbohydrates, van Eijck and Kroon [14] calculated hypothetical crystal structures for several conformations of D-iditol, D-mannitol and D-glucitol in a number of experimental space groups. In their force field UNITAT, the crystal structures had relative energies between 0 and 3 kJ/mole and rankings between 1 and 7, all with respect to the calculated structures with lowest energy. Although the preliminary results are promising, application of the method with the aim to trace polymorphic modifications is met with serious problems particulary related to structures with more than one molecule in the asymmetric unit.

Therefore, to extend the structural data of D-glucitol we undertook the crystal structure analyses of D-glucitol 2/3-hydrate (**1**) and *epsilon* D-glucitol (**2**) with the emphasis on the phenomenon of conformational polymorphism.

2. Experimental

Colourless needle-shaped crystals of **1** (about 10 mm long) and **2** (3–4 mm long) were obtained, respectively, after cooling at 298 K, a 70% (m/m) D-sorbitol aq solution (**1**) and by slow evaporation from a 98% (v/v) EtOH/water solution (**2**), and used for X-ray structural analyses at 100 K. The structures were solved by direct methods with the program SHELXS-96 [15] and refined on F^2 against all unique reflections with the program SHELXL-96 [16]; the validated threshold $F > 4\sigma(F)$ was used for calculating $R_{1(\mathrm{obs})}$ only. Intensities were corrected for Lorentz and polarization effects, but not for absorption. The configurations were selected to comply with the known chirality. Crystallographic data of interest for **1** and **2** are summarized in Table 1. The non-water hydrogens of **1** and the non-hydroxyl hydrogens of **2** were introduced at theoretical positions and refined riding on their carrier atoms; the water hydrogens were refined with a O–H distance restraint and the hydroxyl hydrogens of **2** were refined without any restraints. The last refinement cycles were performed using anisotropic thermal parameters for the non-hydrogen atoms. The hydrogen atoms were assigned constant isotropic thermal parameters equal to the equivalent thermal parameters of their carrier atoms multiplied by a factor of 1.5, except for hydrogens attached to carbon atoms where a factor of 1.2 was used.

3. Results and discussion

The asymmetric unit of D-glucitol 2/3-hydrate (**1**) consists of three glucitol molecules and two molecules of water and that of *epsilon* D-glucitol (**2**) of two molecules. A representation of the symmetry independent molecules **1A**, **1B** and **1C** and **2A** and **2B** is shown in Figs. 1 and 2, respectively. The program package EUCLID [17] was used for the calculation of geometries and to obtain the

Table 1
Crystallographic data for **1** and **2**[a,b]

	1	**2**
Formula	$C_6H_{14}O_6\cdot(H_2O)_{2/3}$	$C_6H_{14}O_6$
Molecular weight	194.18	182.17
Crystal size (mm)	0.75×0.20×0.15	0.65×0.15×0.10
Crystal system	Triclinic	Monoclinic
Space group	$P1$	$P2_1$
Z	3	4
a (Å)	4.7845(1)	4.7907(1)
b (Å)	8.7663(1)	9.4884(1)
c (Å)	16.3329(1)	17.7307(1)
α (°)	101.134(1)	90
β (°)	96.113(1)	94.446(1)
γ (°)	95.870(1)	90
V (Å^3)	663.01(2)	803.54(2)
D_c (g cm^{-3})	1.459	1.506
$F(000)$	314	392
μ (cm^{-1})	1.44	1.46
$2\theta_{\max}$ (°)	55.05	55.04
R_{int} (on F^2)	0.042	0.082
Data collection *hkl*-range	$-4\leq6$; $-10\leq11$; $-19\leq21$	$-6\leq6$; $-12\leq7$; $-22\leq22$
Reflections measured	4279	5635
Unique reflections (n)	3497	2662
Reflections with ($F > 4\sigma(F)$)	3399	2504
Number of parameters (p)	374	254
$R_{1(\mathrm{obs})}$ (on F)[c]	0.034	0.050
$R_{1(\mathrm{all})}$ (on F)[c]	0.036	0.055
$wR_{2(\mathrm{all})}$ (on F^2)[d,e]	0.091	0.120
Goodness of fit S[f]	1.07	1.19
Extinction parameter		0.007(3)
$(\Delta/\sigma)_{\mathrm{av}}$, $(\Delta/\sigma)_{\max}$	0.002, 0.013	0.001, 0.011
$\Delta\rho$(eÅ^{-3})	$-0.24\leq0.30$	$-0.27\leq0.41$

[a] Standard deviations in parentheses.

[b] Diffractometer Nonius KappaCCD, $\lambda(\mathrm{Mo}\ K_a) = 0.71073$ Å, $T = 100$ K.

[c] $R_1 = \Sigma \parallel F_o| - |F_c \parallel / \Sigma|F_o|$.

[d] $wR_2 = [\Sigma w(F_o^2 - F_c^2)^2 / \Sigma w(F_o^2)^2]^{1/2}$.

[e] **1**: $w = 1/[\sigma^2(F_o^2) + (0.0625P)^2 + 0.1586P]$ where $P = (F_o^2 + 2F_c^2)/3$;
2: $w = 1/[\sigma^2(F_o^2) + (0.0296P)^2 + 0.9344P]$ where $P = (F_o^2 + 2F_c^2)/3$.

[f] $S = [\Sigma w(F_o^2 - F_c^2)^2/(n-p)]^{1/2}$.

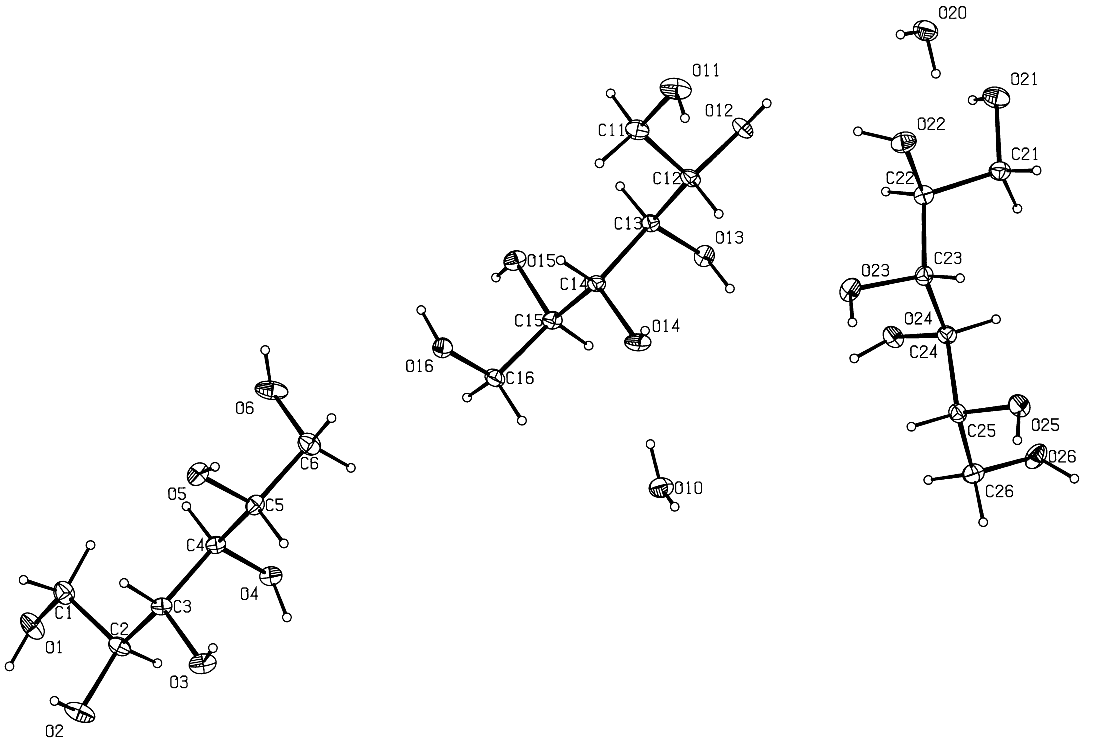

Fig. 1. ORTEP plot of the asymmetric unit of the glucitol hydrate (**1**). Thermal ellipsoids at 50% probability.

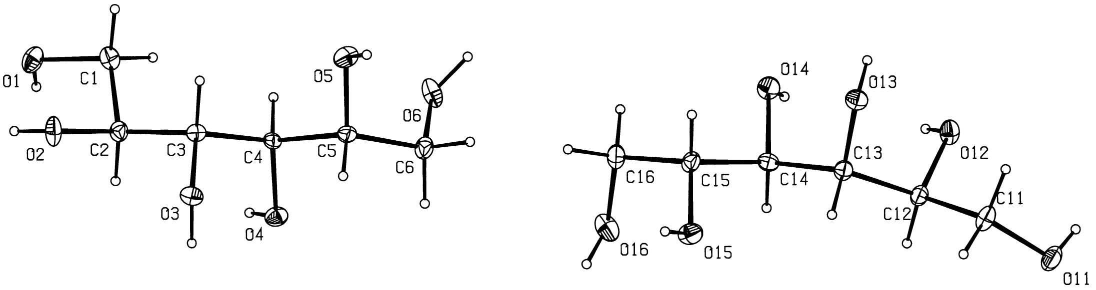

Fig. 2. ORTEP plot of the asymmetric unit of epsilon glucitol (**2**). Thermal ellipsoids at 50% probability.

representations which depict the anisotropic temperature factors[1]. The positional and equivalent isotropic thermal parameters for the non-hydrogen atoms are listed in Table 2. The bent-chain conformation as found in the *A* form [*MAA*(*AA*)][2] of D-glucitol and in the glucitol-pyridine complex [*MAA*(*MP*)] is also present in the three independent molecules of **1** [*MAA*(*AP*)] and in one of the independent molecules of **2** [*MAA*(*AP*)], respectively. As shown by the notations, the conformers nevertheless adopt distinct orientations of the terminal hydroxyl groups. The second independent molecule (**2B**) surprisingly adopts an extended-chain conformation [*AAA*(*AP*)]. The notations clearly show that the *A* and *epsilon* forms constitute the first genuine conformational polymorphs in the class of alditols. The [*AAA*(*AP*)] form of **2** has a parallel C-2–O-2//C-4–O-4 interaction with a distance between O-2 and O-4 of 3.104 Å and a dihedral angle of 5.87°. The carbon chain is slightly curved and deviates from planarity

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[1] Tables of atomic coordinates, anisotropic thermal parameters, bond lengths, and bond angles have been deposited with and can be obtained, on request, from the Director, Cambridge Crystallographic Data Centre, 12 Union Road, Cambridge, CB2 1EZ, UK: deposition number: 102887 for *epsilon* D-glucitol; 102887 for D-glucitol 2/3-hydrate.

[2] *M* = *Msc*, *P* = *Psc* and *A* = *ap* [18] refer to torsion angles of −60, +60 and 180°, respectively. In order to describe the conformations of the carbon chain as well as those of the terminal hydroxyl groups, the following notation will be used: the first three capitals denote the *carbon chain* conformation and the two capitals between parentheses the *terminal* OH orientation with respect to the carbon chain.

Table 2
Fractional positional parameters of C and O atoms and equivalent thermal parameters (Å^2) for **1** and **2**[a]

Atom	x	y	z	U_{eq}[b]	Atom	x	y	z	U_{eq}[b]
1A									
C-1	1.1067(5)	−0.5502(3)	1.4657(1)	0.0149(6)	O-22	0.0612(3)	0.5841(2)	0.7818(1)	0.0171(4)
C-2	1.2232(4)	−0.6194(2)	1.3852(1)	0.0124(5)	O-23	0.1465(3)	0.2733(2)	0.77680(9)	0.0155(4)
C-3	1.4192(4)	−0.4958(2)	1.3565(1)	0.0104(5)	O-24	−0.4111(3)	0.1233(2)	0.71592(9)	0.0131(4)
C-4	1.2613(4)	−0.3691(2)	1.3258(1)	0.0106(5)	O-25	0.0575(3)	0.0988(2)	0.5532(1)	0.0159(4)
C-5	1.4636(4)	−0.2451(2)	1.2999(1)	0.0112(5)	O-26	−0.5199(3)	−0.0726(2)	0.5187(1)	0.0176(5)
C-6	1.3081(5)	−0.1191(3)	1.2694(1)	0.0155(6)	O-10 (water)	1.3684(4)	−0.0499(2)	0.8838(1)	0.0168(4)
O-1	0.8955(3)	−0.6578(2)	1.4867(1)	0.0182(5)	O-20 (water)	0.8252(4)	0.9172(2)	0.7994(1)	0.0183(4)
O-2	1.3668(4)	−0.7495(2)	1.3990(1)	0.0191(5)	**2A**				
O-3	1.5505(3)	−0.5763(2)	1.2892(1)	0.0151(4)	C-1	0.1714(6)	0.1846(4)	0.6488(2)	0.0143(8)
O-4	1.0473(3)	−0.4365(2)	1.25689(9)	0.0126(4)	C-2	0.3282(5)	0.0488(4)	0.6404(2)	0.0108(8)
O-5	1.6693(3)	−0.1799(2)	1.37113(9)	0.0137(4)	C-3	0.4784(5)	0.0380(4)	0.5672(2)	0.0096(8)
O-6	1.1481(3)	−0.0464(2)	1.3320(1)	0.0199(5)	C-4	0.2741(5)	0.0312(4)	0.4951(2)	0.0090(8)
1B					C-5	0.4414(5)	0.0337(4)	0.4249(2)	0.0104(8)
C-11	1.6048(5)	0.6963(2)	1.0542(1)	0.0148(6)	C-6	0.2535(6)	0.0163(4)	0.3518(2)	0.0137(8)
C-12	1.4059(4)	0.5962(2)	0.9805(1)	0.0113(5)	O-1	0.0577(5)	0.1889(3)	0.7212(1)	0.0162(8)
C-13	1.2192(4)	0.4634(2)	1.0046(1)	0.0097(5)	O-2	0.5480(4)	0.0409(3)	0.7019(1)	0.0162(8)
C-14	1.3842(4)	0.3390(2)	1.0352(1)	0.0097(5)	O-3	0.6610(4)	−0.0812(3)	0.5718(1)	0.0126(6)
C-15	1.1899(4)	0.2205(2)	1.0674(1)	0.0108(5)	O-4	0.1184(4)	−0.0954(3)	0.4917(1)	0.0127(6)
C-16	1.3475(4)	0.0994(2)	1.1023(1)	0.0130(5)	O-5	0.5939(4)	0.1625(3)	0.4256(1)	0.0148(6)
O-11	1.7757(3)	0.8174(2)	1.0296(1)	0.0196(5)	O-6	0.0398(4)	0.1225(3)	0.3438(1)	0.0167(8)
O-12	1.2197(3)	0.6945(2)	0.94759(9)	0.0137(4)	**2B**				
O-13	1.0044(3)	0.3919(2)	0.93674(9)	0.0125(4)	C-11	0.9149(6)	−0.1448(4)	−0.1776(2)	0.0150(8)
O-14	1.5046(3)	0.2533(2)	0.9672(1)	0.0142(4)	C-12	0.7355(6)	−0.0959(4)	−0.1149(2)	0.0113(8)
O-15	1.0544(3)	0.3082(2)	1.13159(9)	0.0131(4)	C-13	0.9251(6)	−0.0589(4)	−0.0432(2)	0.0110(8)
O-16	1.5723(3)	0.1675(2)	1.16794(9)	0.0126(4)	C-14	0.7620(6)	−0.0361(4)	0.0273(2)	0.0107(8)
1C					C-15	0.9591(6)	−0.0433(4)	0.1002(2)	0.0118(8)
C-21	−0.3256(5)	0.5172(2)	0.6723(1)	0.0144(5)	C-16	0.7976(6)	−0.0258(4)	0.1708(2)	0.0150(8)
C-22	−0.1522(4)	0.4585(2)	0.7407(1)	0.0115(5)	O-11	0.7496(5)	−0.2087(3)	−0.2393(1)	0.0193(8)
C-23	−0.0133(4)	0.3134(2)	0.7065(1)	0.0114(5)	O-12	0.5723(4)	0.0228(3)	−0.1439(1)	0.0137(5)
C-24	−0.2305(4)	0.1744(2)	0.6598(1)	0.0111(5)	O-13	1.1056(4)	0.0576(3)	−0.0558(1)	0.0124(6)
C-25	−0.0851(4)	0.0387(2)	0.6153(1)	0.0116(5)	O-14	0.6324(5)	0.1003(3)	0.0267(1)	0.0136(6)
C-26	−0.2963(5)	−0.1051(2)	0.5754(1)	0.0154(6)	O-15	1.1005(5)	−0.1761(3)	0.1009(1)	0.0156(6)
O-21	−0.4675(3)	0.6449(2)	0.7068(1)	0.0182(5)	O-16	0.6128(4)	−0.1428(3)	0.1797(1)	0.0178(8)

[a] Standard deviations in parentheses.
[b] $U_{eq} = (\Sigma_i \Sigma_j U_{ij} a_i^* a_j^* a_i \cdot a_j)/3$.

Table 3
Torsion angles (°) for **1** and **2**[a,b]

	1A	**1B**	**1C**	**2A**	**2B**
C-1–C-2–C-3–C-4	−68.5(2)	−64.9(2)	−59.3(2)	−66.7(4)	−168.9(3)
C-2–C-3–C-4–C-5	178.4(1)	173.6(1)	171.8(1)	175.1(3)	163.2(3)
C-3–C-4–C-5–C-6	−180.0(1)	−177.2(1)	174.9(1)	175.8(3)	−178.1(3)
O-1–C-1–C-2–C-3	172.1(2)	179.6(2)	175.9(2)	−175.5(2)	167.5(3)
O-2–C-2–C-3–C-4	169.7(1)	175.7(1)	−178.8(1)	174.9(3)	71.6(4)
C-1–C-2–C-3–O-3	171.2(2)	169.7(2)	178.8(2)	169.1(2)	63.8(4)
O-3–C-3–C-4–C-5	−62.4(2)	−60.9(2)	−68.3(2)	−61.7(4)	−69.4(4)
C-2–C-3–C-4–O-4	−59.0(2)	−67.9(2)	−63.8(2)	−67.1(4)	−78.3(4)
O-4–C-4–C-5–C-6	56.4(2)	62.6(2)	50.9(2)	54.9(4)	60.4(4)
C-3–C-4–C-5–O-5	−57.4(2)	−55.9(2)	−63.6(2)	−60.9(3)	−56.1(4)
C-4–C-5–C-6–O-6	56.2(2)	56.2(2)	55.1(2)	57.2(4)	66.4(4)
O-1–C-1–C-2–O-2	−64.6(2)	−61.6(2)	−63.1(2)	−58.3(3)	−69.8(4)
O-2–C-2–C-3–O-3	49.3(2)	50.2(2)	59.3(2)	50.7(3)	−55.7(3)
O-3–C-3–C-4–O-4	60.2(2)	57.5(2)	56.1(2)	56.1(3)	49.0(3)
O-4–C-4–C-5–O-5	179.0(2)	−176.0(1)	172.4(1)	178.2(2)	−177.6(2)
O-5–C-5–C-6–O-6	−63.9(2)	−63.2(2)	−63.2(2)	−63.9(3)	−53.7(3)

[a] Standard deviations in parentheses.
[b] Atom numbering for **B** and **C** can be derived from those of **A** by adding 10 and 20, respectively.

($\sigma_{\text{plane}} = 0.210$) as illustrated by the deviations from the best plane of −0.178(4), −0.021(4), 0.236(4), 0.138(4), −0.014(4) and −0.160(4) Å, respectively. The C–C bonds in **1** range from 1.517(3) to 1.540(3) Å (mean 1.530 Å) and in **2** from 1.505(5) to 1.550(5) Å (mean 1.534 Å). The trend towards shorter terminal C–C bonds has also been observed in some alditols and glucitol derivatives [7,19,20]. The C–O bonds in **1** range from 1.419(3) to 1.435(2) Å (mean 1.428 Å) and in **2** from 1.413(4) to 1.458(4) Å (mean 1.433 Å). The C–C–C angles in **1** range from 111.4(2) to 114.2(2)° (mean 112.5°) and in **2** from 109.4(2) to 114.3(3)° (mean 111.8°). The C–C–O angles in **1** range from 105.8(1) to 113.3(1)° (mean 109.8°) and in **2** from 105.7(2) to 112.1(3)° (mean 109.8°). These results all compare well with the average values found from X-ray studies of other alditols, and the same holds for the torsion angles which are tabulated in Table 3. The hydrogen-bond geometries are given in Table 4. When the O–H distances are normalized to 0.97 Å, to correct for the well-known electron displacement from the H nucleus, the H···O distances have a normal range of 1.70 to 1.93 Å [average 1.80(5) Å]. No anomalies such as found in the neutron diffraction analysis of the *A* form of D-glucitol [2] were observed.

Table 4
Hydrogen-bond geometries (distances in Å, angles in °) for **1** and **2**[a]

Donor–H··· Acceptor	Symmetry operation[b]	*D–H*[c]	*H···A*[c]	*D···A*	*D-H···A*
1					
O-1–H···O-25	1.646	0.8398	1.9298	2.718(2)	155.87
O-2–H···O-1	1.655	0.8400	1.8964	2.732(2)	173.04
O-3–H···O-4	1.655	0.8398	1.8847	2.711(2)	167.81
O-4–H···O-15	1.545	0.8403	1.9675	2.731(2)	150.67
O-5–H···O-6	1.655	0.8395	1.8243	2.660(2)	173.87
O-6–H···O-2	1.565	0.8402	1.8419	2.677(2)	172.25
O-11–H···O-12	1.655	0.8397	1.9871	2.826(2)	176.39
O-12–H···O-10	1.565	0.8403	1.9265	2.710(2)	154.73
O-13–H···O-23	1.655	0.8399	2.0020	2.800(2)	158.44
O-14–H···O-13	1.655	0.8401	1.8756	2.708(2)	170.80
O-15–H···O-16	1.455	0.8398	1.8714	2.681(2)	161.42
O-16–H···O-3	1.565	0.8404	1.9534	2.711(2)	149.52
O-21–H···O-22	1.455	0.8392	1.9110	2.732(2)	165.69
O-22–H···O-12	1.455	0.8395	1.9251	2.692(2)	151.25
O-23–H···O-24	1.655	0.8398	1.9384	2.777(2)	175.98
O-24–H···O-20	1.445	0.8393	1.9086	2.728(2)	165.02
O-25–H···O-26	1.655	0.8409	1.8436	2.683(2)	176.46
O-26–H···O-5	1.354	0.8393	1.8776	2.698(2)	165.20
O-10–H···O-14	1.555	0.81(3)	1.91(3)	2.721(2)	171(3)
O-10–H···O-20	1.645	0.79(3)	1.93(3)	2.716(3)	174(4)
O-20–H···O-21	1.655	0.80(3)	1.96(3)	2.724(2)	159(3)
O-20–H···O-10	1.565	0.82(3)	1.95(3)	2.769(3)	174(3)
2					
O-1–H···O-2	1.455	0.81(5)	2.00(5)	2.815(3)	175(4)
O-2–H···O-12	1.556	0.75(5)	2.10(5)	2.733(3)	142(4)
O-3–H···O-5	2.646	0.88(5)	1.85(5)	2.723(4)	172(4)
O-4–H···O-3	1.455	0.81(4)	1.90(4)	2.705(3)	171(5)
O-5–H···O-6	1.655	0.81(4)	1.91(4)	2.700(3)	166(5)
O-6–H···O-11	2.655	0.87(5)	1.84(5)	2.703(3)	167(5)
O-11–H···O-2	1.554	0.70(6)	2.06(6)	2.734(4)	161(6)
O-12–H···O-13	1.455	0.78(4)	2.06(4)	2.844(3)	176(5)
O-13–H···O-15	2.755	0.83(5)	2.00(5)	2.807(4)	164(4)
O-14–H···O-13	1.455	0.67(5)	2.18(5)	2.846(3)	169(6)
O-15–H···O-16	1.655	0.79(4)	1.97(4)	2.747(3)	169(6)
O-16–H···O-1	2.646	0.86(5)	1.97(5)	2.775(3)	156(5)

[a] Standard deviations in parentheses.

[b] The symmetry operation is performed on the acceptor atom *A*. The first digit indicates one of the following symmetry operations: (1) x, y, z; (2) $-x, 0.5+y, -z$. The last three digits specify the lattice translations, e.g. 1.645 is *a–b* translated from 1.555.

[c] No standard deviations are given for H atoms at calculated theoretical positions.

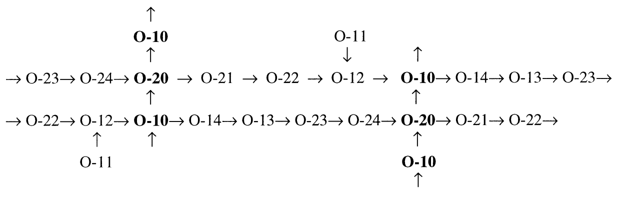
The conformers of **1** and **2** are exceptions to the general rule in the alditols, that each hydroxyl is involved as a hydrogen-bond donor and acceptor. Though the hydroxyls all act as donor, O-11 in **1B**, O-4 in **2A** and O-14 in **2B** do not accept hydrogen bonds; this is compensated for by O-12 in **1B**, O-2 in **2A** and O-13 in **2B**, respectively, which do accept two hydrogen bonds.

The hydrogen-bond schemes of **1** and **2** illustrate a high degree of cooperativity. The hydrogen-bond scheme of D-glucitol 2/3-hydrate (**1**) is complicated and consists of four infinite chains. Two chains are independent, one is built up by molecules **1A** and **1C**, the other one by molecules **1A** and **1B**.

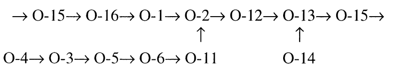
→O-1→O-25→O-26→O-5→O-6→O-2→O-1→

→O-3→O-4→O-15→O-16→O-3→

Two sequences of the larger third chain are cross-linked by a fourth chain of donor–acceptor hydrogen bonds of the two independent water molecules. Curiously, this cross-linked pattern contains only molecules **1B** and **1C**.



In contrast, the hydrogen-bond scheme of *epsilon* D-glucitol (**2**) is simpler and resembles that of the hexitol D-iditol [21] in that it consists of an infinite chain which is joined by a finite one.



The pattern of hydrogen bonds of the polymorphic *A* form [2] can be visualised as a system of two separate infinite chains. Like in the other hexitols, all hydrogen bonds in structures **1** and **2** are intermolecular [22] and one is tempted to speculate whether the variability of hydrogen-bond patterns may be operative in the formation of other polymorphs.

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References

[1] J.W. Du Ross, *Pharm. Technol.*, 8 (1984) 42–52.

[2] Y.J. Park, G.A. Jeffrey, and W.C. Hamilton, *Acta Crystallogr. Sect. B*, 27 (1971) 2393–2401.

[3] H.S. Kim, G.A. Jeffrey, and R.D. Rosenstein, *Acta Crystallogr. Sect. B*, 27 (1971) 307–314.

[4] F.H. Allen, O. Kennard, and R. Taylor, *Acc. Chem. Res.*, 16 (1983) 146–153.

[5] G.A. Jeffrey, *Acta Crystallogr. Sect. B*, 46 (1990) 89–103.

[6] W. Pigman, *The Carbohydrates: Chemistry, Biochemistry and Physiology*, Academic Press, New York, 1957.

[7] G.A. Jeffrey and H.S. Kim, *Carbohydr. Res.*, 14 (1970) 207–216.

[8] H.M. Berman, G.A. Jeffrey, and R.D. Rosenstein, *Acta Crystallogr. Sect. B*, 24 (1968) 442–449.

[9] H.S. Kim, G.A. Jeffrey, and R.D. Rosenstein, *Acta Crystallogr. Sect. B*, 24 (1968) 1449–1455.

[10] S.J. Angyal, J.K. Saunders, C.T. Grainger, R. Le Fur, and P.G. Williams, *Carbohydr. Res.*, 150 (1986) 7–21.

[11] P. Köll, M. Bischoff, C. Bretzke, and J. Kopf, *Carbohydr. Res.*, 262 (1994) 1–8.

[12] J. Kopf, M. Morf, B. Hagen, M. Bischoff, and P. Köll, *Carbohydr. Res.*, 262 (1994) 9–25.

[13] P. Köll, R. Bruns, and J. Kopf, *Carbohydr. Res.*, 305 (1998) 147–154.

[14] B.P. van Eijck and J. Kroon, *J. Comput. Chem.*, submitted.

[15] G.M. Sheldrick, SHELXS-96, *Program for Structure Solution*, University of Göttingen, Germany, 1996.

[16] G.M. Sheldrick, SHELXL-96, *Program for Structure Refinement*, University of Göttingen, Germany, 1996.

[17] A.L. Spek, *Acta Crystallogr. Sect. A*, 46 (1990) C-34.

[18] W. Klyne and V. Prelog, *Experientia*, 16 (1960) 521–523.

[19] J.A. Kanters, G. Roelofsen, and D. Smits, *Acta Crystallogr. Sect. B*, 33 (1977) 3635–3640.

[20] J.A. Kanters, A. Schouten, and M. van Bommel, *Journal of Molecular Structure*, 238 (1990) 403–412.

[21] N. Azarnia, G.A. Jeffrey, and M.S. Shen, *Acta Crystallogr. Sect. B*, 28 (1972) 1007–1013.

[22] G.A. Jeffrey, *Carbohydr. Res.*, 28 (1973) 233–241.